

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/595,562
Source: IFWP
Date Processed by STIC: 2/1/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/595,562

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- Numbering
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) 1,2,3,56,61,69 contain h's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid "bug" sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence. (NEW RULES)
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing. (NEW RULES)
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220> Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

Please consult Sequence Rules
for VALID format



IFWP

RAW SEQUENCE LISTING

DATE: 02/01/2007

PATENT APPLICATION: US/10/595,562

TIME: 12:08:51

Input Set : A:\PTO.SS.TXT

Output Set: N:\CRF4\02012007\J595562.raw

Does Not Comply
Corrected Diskette Needed

see pp 1-9

3 <110> APPLICANT: Medvet Science, Pty Ltd
4 Guthridge, Mark
5 Ramshaw, Hayley
6 Stomski, Frank
7 Felquer, Fernando
8 Lopez, Angel
10 <120> TITLE OF INVENTION: A Bidentate Motif and Methods of Use
W--> 12 <130> FILE REFERENCE:
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/595,562
C--> 14 <141> CURRENT FILING DATE: 2006-04-27
14 <160> NUMBER OF SEQ ID NOS: 71
16 <170> SOFTWARE: PatentIn version 3.3

ERRORED SEQUENCES

insert this mandatory numeric identifier and
response

18 <210> SEQ ID NO: 1 <211> 10
19 <212> TYPE: PRT
20 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: misc_feature
25 <222> LOCATION: (2)..(3)
26 <223> OTHER INFORMATION: Xaa can be any residue
28 <220> FEATURE:
29 <221> NAME/KEY: misc_feature
30 <222> LOCATION: (5)..(5)
31 <223> OTHER INFORMATION: Xaa (1-13 repeats) can be any residue
33 <220> FEATURE:
34 <221> NAME/KEY: misc_feature
35 <222> LOCATION: (6)..(6)
36 <223> OTHER INFORMATION: Xaa can be Arg, Lys, His or Gln
38 <220> FEATURE:
39 <221> NAME/KEY: misc_feature
40 <222> LOCATION: (7)..(7)
41 <223> OTHER INFORMATION: Xaa (2-3 repeats) can be any residue or a hydrophobic residue
or an
42 equivalent thereof
44 <220> FEATURE:
45 <221> NAME/KEY: misc_feature
46 <222> LOCATION: (8)..(8)
47 <223> OTHER INFORMATION: Xaa is serine or threonine
49 <220> FEATURE:
50 <221> NAME/KEY: misc_feature
51 <222> LOCATION: (9)..(9)

variable length is not permitted - see item 5
on Err
summary
sheet

see item 5 on Err summary sheet

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52 <223> OTHER INFORMATION: Xaa can be any residue

54 <400> SEQUENCE: 1

W--> 56 Asn Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Pro

E--> 57 1

5

10

60 <210> SEQ ID NO: 2

61 <212> TYPE: PRT

62 <213> ORGANISM: Homo sapiens

65 <220> FEATURE:

66 <221> NAME/KEY: misc_feature

67 <222> LOCATION: (2)..(2)

68 <223> OTHER INFORMATION: Xaa (1-16 repeats) can be any residue

70 <220> FEATURE:

71 <221> NAME/KEY: misc_feature

72 <222> LOCATION: (3)..(3)

73 <223> OTHER INFORMATION: Xaa can be Arg, Lys, His or Gln

75 <220> FEATURE:

76 <221> NAME/KEY: misc_feature

77 <222> LOCATION: (4)..(4)

78 <223> OTHER INFORMATION: Xaa (2-3 repeats) can be any residue or a hydrophobic residue

or an

79 equivalent thereof

81 <220> FEATURE:

82 <221> NAME/KEY: misc_feature

83 <222> LOCATION: (5)..(5)

84 <223> OTHER INFORMATION: Xaa is serine or threonine

86 <220> FEATURE:

87 <221> NAME/KEY: misc_feature

88 <222> LOCATION: (6)..(6)

89 <223> OTHER INFORMATION: Xaa can be any residue

92 <400> SEQUENCE: 2

W--> 94 Tyr Xaa Xaa Xaa Xaa Xaa Xaa Pro

E--> 95 1

5

98 <210> SEQ ID NO: 3

99 <212> TYPE: PRT

100 <213> ORGANISM: Homo sapiens

103 <220> FEATURE:

104 <221> NAME/KEY: misc_feature

105 <222> LOCATION: (2)..(3)

106 <223> OTHER INFORMATION: Xaa can be any residue

108 <220> FEATURE:

109 <221> NAME/KEY: misc_feature

110 <222> LOCATION: (4)..(4)

111 <223> OTHER INFORMATION: Tyr is phosphotyrosine

113 <220> FEATURE:

114 <221> NAME/KEY: misc_feature

115 <222> LOCATION: (5)..(5)

116 <223> OTHER INFORMATION: Xaa (1-30 repeats) can be any residue

118 <220> FEATURE:

RAW SEQUENCE LISTING

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Input Set : A:\PTO.SS.TXT

Output Set: N:\CRF4\02012007\J595562.raw

119 <221> NAME/KEY: misc_feature
 120 <222> LOCATION: (6)..(6)
 121 <223> OTHER INFORMATION: Xaa can be Arg, Lys, His or Gln
 123 <220> FEATURE:
 124 <221> NAME/KEY: misc_feature
 125 <222> LOCATION: (7)..(7)
 126 <223> OTHER INFORMATION: Xaa (1-4 repeats) can be any residue
 128 <220> FEATURE:
 129 <221> NAME/KEY: misc_feature
 130 <222> LOCATION: (8)..(8)
 131 <223> OTHER INFORMATION: Xaa is phosphoserine or phosphothreonine
 133 <220> FEATURE:
 134 <221> NAME/KEY: misc_feature
 135 <222> LOCATION: (9)..(9)
 136 <223> OTHER INFORMATION: Xaa can be any residue

138 <400> SEQUENCE: 3 / / / /
 W--> 140 Asn Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa

E--> 141 1 5
 144 <210> SEQ ID NO: 4 → C211714
 145 <212> TYPE: PRT
 146 <213> ORGANISM: Homo sapiens

148 <400> SEQUENCE: 4
 E--> 150 Asn Gly Pro Tyr Leu Gly.....Pro Pro...His Ser Arg Ser Leu Pro
 E--> 151 1 5

154 <210> SEQ ID NO: 5 → C211713
 155 <212> TYPE: PRT
 156 <213> ORGANISM: Homo sapiens

158 <400> SEQUENCE: 5
 E--> 160 Asn Val His Tyr Arg Thr.....Pro...Lys Thr His Thr Met Pro
 E--> 161 1 5

164 <210> SEQ ID NO: 6 → C211715
 165 <212> TYPE: PRT
 166 <213> ORGANISM: Homo sapiens

168 <400> SEQUENCE: 6
 E--> 170 Arg Tyr Phe Thr Gln Lys Glu Glu.....Thr Glu Ser Gly Ser Gly Pro
 E--> 171 1 5 5 10 15

174 <210> SEQ ID NO: 7 → C211722
 175 <212> TYPE: PRT
 176 <213> ORGANISM: Homo sapiens

178 <400> SEQUENCE: 7
 E--> 180 Asn Lys Lys Tyr Glu Leu Gln Asp Arg Asp Val Cys Glu.....Pro...Arg Tyr
 181 1 5 10 15

E--> 184 Arg Ser Val Ser Glu Pro
 188 <210> SEQ ID NO: 8 → 20

these are invalid. If you are denoting a gap, delete the 2 Pro's, and begin a new SEQ ID NO with this group. Otherwise, number the amino acids.

same error

same error

same error

RAW SEQUENCE LISTING

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Input Set : A:\PTO.SS.TXT

Output Set : N:\CRF4\02012007\J595562.raw

211713

189 <212> TYPE: PRT

190 <213> ORGANISM: Homo sapiens

192 <400> SEQUENCE: 8

E--> 194 Asn Pro Thr Tyr Ser Val Met.....Arg Ser His Ser Tyr Pro

E--> 195 1 5 10

198 <210> SEQ ID NO: 9 } 211724

199 <212> TYPE: PRT

200 <213> ORGANISM: Homo sapiens

202 <400> SEQUENCE: 9

E--> 204 Asn Ile Phe Tyr Leu Ile Arg.....Lys Ser Gly Ser Phe Pro Met Pro Glu

E--> 205 1 5 10 15

E--> 208 Leu Lys Leu Ser Ile Ser Phe Pro

212 <210> SEQ ID NO: 10 } 211719

213 <212> TYPE: PRT

214 <213> ORGANISM: Homo sapiens

216 <400> SEQUENCE: 10

E--> 218 Asn Glu Glu Tyr Leu Asp Leu Ser Gln.....Pro Leu Glu Gln Tyr Ser Pro

E--> 219 1 5 10 15

E--> 222 Ser Tyr Pro

226 <210> SEQ ID NO: 11 } 211719

227 <212> TYPE: PRT

228 <213> ORGANISM: Homo sapiens

230 <400> SEQUENCE: 11

E--> 232 Asn Gln Glu Tyr Leu Asp Leu Ser Met.....Pro Leu Asp Gln Tyr Ser Pro

E--> 233 1 5 10 15

E--> 236 Ser Phe Pro

240 <210> SEQ ID NO: 12 } 211716

241 <212> TYPE: PRT

242 <213> ORGANISM: Homo sapiens

244 <400> SEQUENCE: 12

E--> 246 Asn Ala Thr Tyr Lys Val Asp.....Val Ile Gln Arg Thr Arg Ser Lys Pro

E--> 247 1 5 10 15

250 <210> SEQ ID NO: 13 } 211711

251 <212> TYPE: PRT

252 <213> ORGANISM: Homo sapiens

254 <400> SEQUENCE: 13

E--> 256 Asn Pro Glu Tyr.....His Ser Ala Ser Ser Gly Pro

E--> 257 1 5 10

260 <210> SEQ ID NO: 14 } 21710

261 <212> TYPE: PRT

262 <213> ORGANISM: Homo sapiens

264 <400> SEQUENCE: 14

RAW SEQUENCE LISTING

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TIME: 12:08:51

Input Set : A:\PTO.SS.TXT

Output Set: N:\CRF4\02012007\J595562.raw

E--> 266 Asn Pro Asp Tyr.....Trp Asn His Ser Leu Pro
 E--> 267 1 5 10
 270 <210> SEQ ID NO: 15
 271 <212> TYPE: PRT } <211723
 272 <213> ORGANISM: Homo sapiens

 274 <400> SEQUENCE: 15
 E--> 276 Asn Pro Ser Tyr Ser Ser Asn Pro Phe Val Asn Tyr Asn.....Lys Thr Ser
 E--> 277 1 5 10 15
 E--> 280 Ile Cys Ser Lys Ser Asn Pro
 284 <210> SEQ ID NO: 16 20
 285 <212> TYPE: PRT } <211711
 286 <213> ORGANISM: Homo sapiens

 288 <400> SEQUENCE: 16
 E--> 290 Asn Thr Leu Tyr.....Phe Asn Ser Gln Ser Ser Pro
 E--> 291 1 5 10
 294 <210> SEQ ID NO: 17
 295 <212> TYPE: PRT } <211724
 296 <213> ORGANISM: Homo sapiens

 298 <400> SEQUENCE: 17
 E--> 300 Asn Pro Val Tyr Gln Lys Thr Thr Glu Asp Glu Val His Ile....Cys His
 E--> 301 1 5 10 15
 E--> 304 Asn Gln Asp Gly Tyr Ser Tyr Pro 20
 308 <210> SEQ ID NO: 18 } <211724
 309 <212> TYPE: PRT
 310 <213> ORGANISM: Homo sapiens

 312 <400> SEQUENCE: 18
 314 Asn Pro Val Tyr Leu Lys Thr Thr Glu Glu Asp Leu Ser Ile Asp Ile
 315 1 5 10 15
 E--> 318 Gly...Arg His...Ser Ala Ser Val Gly
 341 <210> SEQ ID NO: 20 20
 342 <212> TYPE: PRT
 343 <213> ORGANISM: Homo sapiens
 E--> 345 <211> LENGTH:
 345 <400> SEQUENCE: 20
 E--> 347 Asn Pro Ile Tyr.....Lys Ser Ala Val Thr Thr Val Val
 E--> 348 1
 351 <210> SEQ ID NO: 21
 352 <212> TYPE: PRT
 353 <213> ORGANISM: Homo sapiens
 E--> 355 <211> LENGTH:
 355 <400> SEQUENCE: 21
 E--> 357 Asn Pro Leu Tyr.....Lys Ser Ala Ile Thr Thr Thr Val
 E--> 358 1
 361 <210> SEQ ID NO: 22
 362 <212> TYPE: PRT

same error
as above

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Input Set : A:\PTO.SS.TXT

Output Set: N:\CRF4\02012007\J595562.raw

363 <213> ORGANISM: Homo sapiens
E--> 365 <211> LENGTH:
365 <400> SEQUENCE: 22
E--> 367 Asn Pro Leu Tyr.....Lys Glu Ala Thr Ser Thr Phe Thr
E--> 368 1
371 <210> SEQ ID NO: 23
372 <212> TYPE: PRT
373 <213> ORGANISM: Homo sapiens
E--> 375 <211> LENGTH:
375 <400> SEQUENCE: 23
E--> 377 Asn Pro Leu Tyr.....Arg Lys Pro Ile Ser Thr His Thr
E--> 378 1
381 <210> SEQ ID NO: 24
382 <212> TYPE: PRT
383 <213> ORGANISM: Homo sapiens
E--> 385 <211> LENGTH:
385 <400> SEQUENCE: 24
E--> 387 Asn Pro Leu Tyr.....Arg Gly Ser Thr Ser Thr Phe Lys
E--> 388 1
391 <210> SEQ ID NO: 25
392 <212> TYPE: PRT
393 <213> ORGANISM: Homo sapiens
E--> 395 <211> LENGTH:
395 <400> SEQUENCE: 25
E--> 397 Pro Gly His Tyr Leu.....Arg Cys Asp Ser Thr Gln Pro
E--> 398 1 5
421 <210> SEQ ID NO: 28
422 <212> TYPE: PRT
423 <213> ORGANISM: Homo sapiens
E--> 425 <211> LENGTH:
425 <400> SEQUENCE: 28
E--> 427 His Ser Gly Tyr Arg His Gln Val Pro Ser Val Gln Val Phe.....Ser Arg
E--> 428 1 5 10
E--> 431 Ser Glu Ser Thr Gln Pro
435 <210> SEQ ID NO: 29
436 <212> TYPE: PRT
437 <213> ORGANISM: Homo sapiens
E--> 439 <211> LENGTH:
439 <400> SEQUENCE: 29
E--> 441 Trp Lys Met Tyr Glu Val Tyr Asp Ala.....Lys Ser Lys Ser Val Ser Leu
E--> 442 1 5
E--> 445 Pro
502 <210> SEQ ID NO: 34
503 <212> TYPE: PRT
504 <213> ORGANISM: Homo sapiens
E--> 506 <211> LENGTH:
506 <400> SEQUENCE: 34
E--> 508 Glu Glu Ile Tyr Ile Ile Met.....Gln Ser Cys Trp Ala Phe Asp Ser
E--> 509 Arg

*global
errors*

*same error
in segs. 26, 27*

same error in segs. 30-32

same error in segs. 35-37

RAW SEQUENCE LISTING

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Input Set : A:\PTO.SS.TXT

Output Set: N:\CRF4\02012007\J595562.raw

E--> 510 1 5
 E--> 513 Lys Arg Pro Ser Phe Pro
 547 <210> SEQ ID NO: 38
 548 <212> TYPE: PRT
 549 <213> ORGANISM: Homo sapiens
 E--> 551 <211> LENGTH:
 551 <400> SEQUENCE: 38
 E--> 553 Leu Val Ala Tyr Ile Ala Phe Lys Arg Trp Asn Ser Cys Lys Gln Asn.....
 554 1 5 10 15
 E--> 557Lys Gln Gly Ala Asn Ser Arg Pro Val Asn Gln Thr Pro Pro Pro Glu
 E--> 561 Gly Glu Lys Leu His Ser Asp Ser Gly Ile Ser
 584 <210> SEQ ID NO: 41
 585 <212> TYPE: PRT
 586 <213> ORGANISM: Homo sapiens
 E--> 588 <211> LENGTH:
 588 <400> SEQUENCE: 41
 590 Asn Pro Asn Tyr Thr Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro
 E--> 591 1 5 ~~10~~ 10 ~~15~~ 15
 E--> 594 Trp Thr.....Lys Val Phe Lys Ser Arg Thr Pro Pro
 650 <210> SEQ ID NO: 46 20 25
 651 <212> TYPE: PRT
 652 <213> ORGANISM: Homo sapiens
 E--> 654 <211> LENGTH:
 654 <400> SEQUENCE: 46
 E--> 656 Asn Gln Glu Tyr.....Leu Asp Leu Ser Ile Pro Leu Asp Gln Tyr Ser Pro
 E--> 657 1
 E--> 660 Ser Phe Pro
 664 <210> SEQ ID NO: 47
 665 <212> TYPE: PRT
 666 <213> ORGANISM: Homo sapiens
 E--> 668 <211> LENGTH:
 668 <400> SEQUENCE: 47
 E--> 670 Asn Glu Glu Tyr Leu Asp Leu Ser Gln Pro Leu Glu.....Gln Tyr Ser Pro
 E--> 671 1 5 10
 E--> 674 Ser Tyr
 678 <210> SEQ ID NO: 48
 679 <212> TYPE: PRT
 680 <213> ORGANISM: Homo sapiens
 E--> 682 <211> LENGTH:
 682 <400> SEQUENCE: 48
 E--> 684 Asn Ala Thr Tyr Lys Val Asp Val Ile.....Gln Arg Thr Arg Ser Lys
 E--> 685 Pro
 E--> 686 1 5 10
 689 <210> SEQ ID NO: 49
 690 <212> TYPE: PRT
 691 <213> ORGANISM: Homo sapiens
 E--> 693 <211> LENGTH:
 693 <400> SEQUENCE: 49
 695 Asn Pro Thr Tyr Lys Met Tyr Glu Gly Gly Glu Pro Asp Asp Val Gly

*same**error in segs
39-40**misaligned
has. (see
item 3**on Enon
summary
sheet)**same error in segs 42-45*

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same

| | | | | | | | | | | | | | | | | | | | |
|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|--|
| 696 | 1 | | | 5 | | | | 10 | | | | 15 | | | | | | | |
| E--> | 699 | Gly | Leu | Leu | Asp | Ala | Asp | Phe | Ala | Leu | Asp | Pro | Asp | | Lys | Pro | Thr | Asn | |
| E--> | 700 | | | | 20 | | | | | | 25 | | | | | | | | |
| E--> | 703 | Phe | Thr | Asn | Pro | | | | | | | | | | | | | | |

same error in seqs. 50-55, 57-59.

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Input Set : A:\PTO.SS.TXT

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:31; Line(s) 465

Seq#:34; Line(s) 508

Seq#:48; Line(s) 684

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/595,562

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Input Set : A:\PTO.SS.TXT

Output Set: N:\CRF4\02012007\J595562.raw

L:12 M:201 W: Mandatory field, data missing, <130> FILE REFERENCE
 L:14 M:270 C: Current Application Number differs, Replaced Current Application No
 L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:54 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
 L:57 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:10 SEQ:1
 L:92 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
 L:95 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:7 SEQ:2
 L:138 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
 L:141 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:9 SEQ:3
 L:148 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:150 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:151 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
 L:151 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:4
 L:158 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:160 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:161 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
 L:161 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:5
 L:168 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:170 M:342 E: Invalid Stop Code On Error, STOP CODON:*
 L:170 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:171 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
 L:171 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:14 SEQ:6
 L:178 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:180 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:184 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
 L:184 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:20 SEQ:7
 L:192 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:194 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:195 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
 L:195 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:8
 L:202 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:204 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:205 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
 M:332 Repeated in SeqNo=9
 L:208 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:23 SEQ:9
 L:216 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:218 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:219 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
 L:222 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:18 SEQ:10
 L:230 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:232 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:233 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
 L:236 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:18 SEQ:11
 L:244 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:246 M:333 E: Wrong sequence grouping, Amino acids not in groups!

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L:247 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
L:247 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:15 SEQ:12
L:254 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:256 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:257 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:13
L:257 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:10 SEQ:13
L:264 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:266 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:267 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:267 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:9 SEQ:14
L:274 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:276 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:277 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15
M:332 Repeated in SeqNo=15
L:280 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:22 SEQ:15
L:288 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:290 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:291 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:291 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:10 SEQ:16
L:298 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:300 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:301 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
M:332 Repeated in SeqNo=17
L:304 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:23 SEQ:17
L:312 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:318 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:318 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18
L:318 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:22 SEQ:18
L:345 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:347 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:348 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20
L:348 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:20
L:355 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:357 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:358 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21
L:358 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:21
L:365 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:367 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:368 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:368 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:22
L:375 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:377 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:378 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:378 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:23
L:385 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:387 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:388 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:24
L:388 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:24
L:395 M:282 E: Numeric Field Identifier Missing, <211> is required.

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L:397 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:398 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:25
L:398 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:25
L:405 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:407 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:408 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:26
L:408 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:16 SEQ:26
L:415 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:417 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:418 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27
L:418 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:13 SEQ:27
L:425 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:427 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:428 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:28
M:332 Repeated in SeqNo=28
L:431 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:21 SEQ:28
L:439 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:441 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:442 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:29
L:445 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:16 SEQ:29
L:453 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:455 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:456 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:30
L:456 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:14 SEQ:30
L:463 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:465 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:469 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31
L:469 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:17 SEQ:31
L:477 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:479 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:480 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32
L:480 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:14 SEQ:32
L:506 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:508 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:509 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:34
M:332 Repeated in SeqNo=34
L:513 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:21 SEQ:34
L:521 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:523 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:524 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:524 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:35
L:531 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:533 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:534 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:534 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:10 SEQ:36
L:541 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:543 M:342 E: Invalid Stop Code On Error, STOP CODON:*\br/>L:543 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:544 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:37

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L:544 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:14 SEQ:37
L:551 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:553 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:557 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:557 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:561 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
M:332 Repeated in SeqNo=38
L:561 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:43 SEQ:38
L:568 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:570 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:571 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39
L:571 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:39
L:578 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:580 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:581 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:40
L:581 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:9 SEQ:40
L:588 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:591 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:41
L:594 M:333 E: Wrong sequence grouping, Amino acids not in groups!
M:332 Repeated in SeqNo=41
L:594 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:26 SEQ:41
L:602 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:608 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:609 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42
L:609 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:30 SEQ:42
L:616 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:622 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:623 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43
L:623 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:31 SEQ:43
L:630 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:636 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:636 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
L:636 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:23 SEQ:44
L:644 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:646 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:647 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
L:647 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:45
L:654 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:656 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:657 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
M:332 Repeated in SeqNo=46
L:660 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:18 SEQ:46
L:668 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:670 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:671 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:47
L:674 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:17 SEQ:47
L:682 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:684 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:686 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:15 SEQ:48

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L:693 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:699 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:703 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:35 SEQ:49
L:711 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:717 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:717 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:23 SEQ:50
L:725 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:731 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:731 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:23 SEQ:51
L:739 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:741 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:742 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:52
L:751 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:761 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
L:911 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61 after pos.:0
L:1018 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68 after pos.:0
L:1044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69 after pos.:0
L:1072 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70 after pos.:0
L:1101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71 after pos.:0